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Listing first 45 summaries
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Compugen Ltd
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nonmuscle myosin I	interaptin - slime	hypothetical prote	skeletal myosin -	myosin heavy chain	hypothetical prote	myosin heavy chain	myosin heavy chain	chromosomal protei	myosin heavy chain	giantín - human	giantin - human	hypothetical prote	chromosome segrega	hypothetical prote	paramyosin - Caeno

ALIGNMENTS

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Qy 355 KKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVV 414	Qy 301 MMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSDMQNVL 354	QY 241 TELDQAKLELRSAQKDLQSADQETTSLRKKSDDPPGNLEÞASATNETVSRLVFESÞAPVE 300 : : ::: : : : : : :	QY 181 EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLN 240 	QY 121 LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEV 180	Qy 61 KLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVES 120	QY 1 MPILSLCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQVGKKTIIN 60 :	Query Match 38.4%; Score 919; DB 2; Length 433; Best Local Similarity 40.7%; Pred. No. 1.9e-40; Matches 191; Conservative 87; Mismatches 117; Indels 74; Gaps 6;	A; Relegence number: 20080; MOLD: 99140833 A; Accession: T30807 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-433 <cot> A; Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1 C; Genetics: A; Gene: TRIP A; Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3</cot>	RESULT 1 T30807 TRAF interacting protein - Fugu rubripes C;Species: Fugu rubripes C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Date: 01-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: T30807 R;Cottage, A; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, FEBS Lett. 443, 370-374, 1999 A;Title: Three receptor genes for plasminogen related growth factors in the genome of

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RESULT 3
T25457
hypothetical
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A; Residues: 1-506 <STO>
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; Pred. No. 0.00019;
79; Mismatches 193;
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Best Local Similarity
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C; Species: Caenorhab
C; Date: 15-Oct-1999
C; Accession: T25457
R; Henkhaus, J.; Wohl
                                                                                                                                                                                                                                                                                                        R; Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtu A;Reference number: Z17588; MUID:98139549
A;Accession: T13030
                                                                                                                                                                                                                                                                                                                                                                                                                                                              microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2;
C;Superfamily: RING finger homology
E;188-238/Domain: RING finger homology <RRNJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-425 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Henkhaus, J.; Wohldmann, P. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid
                                                                                                                           A;Cross-references: FlyBase:FBgn0020503C;Keywords: cytoskeleton
                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1690 <LAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 220038
A; Accession: T25457
                                                                                                                                                                        C; Genetics
                                                                                                                                                                                              A;Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A;Experimental source: strain Oregon R
                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VEKLFFDVQRMGGEAEKPPEIDYREEHY-----KLSTSLKVEQEKLGTLNTENKNLKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PILSL---CTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCRIQVGKKTI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATVESLQNAL----NKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIEL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INKLFFDLAQ----EEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLTDKR----REAAKEIEQLKMEVQS----LKRAAQEDAAIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK----EYENLKEARKATGELADRLKK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TVKSLEKKIIREKDKYRQEIPKLQATINHLTISSEETAYLKRELQESKNRLKTCEFYKI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTSSLQGSCSICFEDLKQNDKISAIVCGHIYHHGCISQWIAT--KRQCPSCRRTVPKNGF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               T13030
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
Score 200.5; DB
Pred. No. 0.0085;
73; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 204.5; DB Pred. No. 0.0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 105;
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                                               DB 2;
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50 RIQVGKKTIINKLFFDLAQEEENVLDAEFLKNE----

--LDSVKAQLSQKDREKRDSQAI 103

Conservative

73;

168;

Indels 131;

Gaps

18;

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RESULT 5
742722
male-enhanced antigen-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Uan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42722
C:Accession: T42722
                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:D78270; N:
A; Cross-references: EMBL:D78270; N:
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kondo, M.; Sutou, S.
DNA Seg. 7, 71-82, 1997
A;Title: Cloning and molecular characterization
A;Reference number: Z2Z242; MUID:97217683
A;Accession: T42722
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                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain C; Function:
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                                  LKATKKRLDSEMKELRQELIKLQGEKKTVEVEHSRLQKDMSLVHQQMAELEGHLQSVQKE 762
                                                                                                   DIAVKSNQVEHLQQE-----TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE::::
                                                                                                                              TLEERNATVESLQNALNKAEMLCSTLKKQM-----KFLEQ------RQDET------KQ 151
                                                                                                                                                                                                 DLAQEEENVLDA-EFLKNE-----LDSVKAQLSQKDREKR-----DSQAIIDTLRD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEKSFEESIKNLQEEVTKAKTENLELSTGTQTTIKDLQERLE-----ITNAELQHK---
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                                                                AREEAHRLKCKMKTMEQIELLLQSQRSEVE----EMIRDMGVGQSAVEQLAVYCVSLKKE 207
                                                                                                                                                                ELQREADSREDAIHFLQNEKIVLEVALQSAKSDKEELDRGARRLEEDTEETSGLLEQLRQ 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTTAESRSSTDVVRIGFDGLGGRTKFIQPRD-TTIIRPVPVKSKAKSKQKVRIKTVSSAS
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                                                                                                                                                                                                                                 Similarity 22.,
94; Conservative
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                                                                                                                                                                                                                                                8.0%;
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 LKEA----RKATGELADRLKKDLVSSRSKLKTLNTELDQA 246
                                                                                                                                                                                                                                                                                                                             some role for spermatogenesis
                                                                                                                                                                                                                                   ;08
                                                                                                                                                                                                                                                                                                                                                                               NID:d1096175;
                                                                                                                                                                                                                                 Score 192.5; DB 2;
Pred. No. 0.017;
0; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DLKTLVEAIQVANANISATNAELSTVLEVL 1141
                                                                                                                                                                                                                                                                                                                                                                                 PID:d1020389;
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A;Molecule type: DNA
A;Residues: 1-2139 <GUI>
A;Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB48065.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 15-Oct-1999 #sequence_revision 15-
C;Accession: T18296
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C;Superfamily: myosin heavy chain; myosin motor domain
F;91-780/Domain: myosin motor domain homology <MMO>
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Best Local
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     448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LAQEEENVLDAEFLKNELDSVKAQLSQK-----DREKRDSQAIIDTLRDTLEERNATV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22.1 hes 97; Conservative
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 KQKVRIKTVSSASQPKLD
                                                                            VLGQKQPNRTTAE----SRSSTDVVRIGFDGLGGRTKFIQPRDTTIIRPVPVKSKAKS
                                                                                                                                                                                                                                                              EALQKNLDLAQQEKAKATKDYRAADGELKSLMNELDDVKDQLDKA-----
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                                                                                                                                                                                                                                                                                                                                                        EKLVAKNSENDAEI--DSLKEEKKALE---DEIEKITDDNNKLS-----EEIDSLDRKY 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESL--QNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQPPFGDEIDLNTT-----FDVNTPPTQTSGS-QHCLPKKLCLERARSPMQNVLKKV 357
                                        ERGLKQDSEKEVQRLRVKCQELETKVAEVG--GANVSIAKVKAKYEAEIEELTTEAEDAL
                                                                                                                                                   ARSPMQNVLKKVHKVSKPESQL----
                                                                                                                                                                                                                                                                                                                                     NALLDSKDSDVSMKEKFQDELKVTKDALETEKKNHAETMRLKG----RLEKEAAEVQVRL
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                                                                                                               AQKQKQAYEKKLQELQENDNDFEEYKETADKRINTLSAQK--DDLQKEL----
                                                                                                                                                                                                                          APVEMMNPRLHQPPFGDEIDLNTTFD-----VNTPPTQTSGSQHCLPKKLCLE-----R
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KAKMKAEKKAKTSQKKLD 2049

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C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrocollicing; hyd
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A36014
myosin heavy chain, r
N;Contains: myosin A
RESULT 8
$61477
gyosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Feb-
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A36014; B36014
R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
A;Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain tA;Reference number: A36014; MUID:90349606
A;Status: nucleic acid sequence not shown
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C;Superfamily: myosin heavy chain; myosin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M35012 C;Genetics:
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A; Residues: 1-2017 <KET>
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Best Local
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                                                                                                                                                                                                                                                                                                                                       RCVGELDEEL
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myosin ATPase (EC 3.6.1.32)
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   #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001
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<MAl>
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A;Gene: zip
A;Gene: zip
A;Cross·references: FlyBase:FBgn0005634
A;Cross·references: FlyBase:FBgn0005634
A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: alternative splicing; ATP; nucleotide binding; P-loop
F;135-855/Domain: myosin motor domain homology <MMOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)
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R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D. J. Mol. Biol. 255, 98-109, 1996

J. Mol. Biol. 255, 98-109, 1996

A;Title: Molecular organization and alternative splicing in zipper, the gene A;Reference number: S61477; MUID:96144835

A;Accession: S61477
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A;Residues: 1-1908,'NL',1911-2057 <MAW>
A;Cross-references: EMBL:U35816; NID:g1141789;
C;Genetics:
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A; Accession: S65349
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R:Mansfield, S.G.; Al-Shirawi, D.Y.;
submitted to the EMBL Data Library,
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A; Residues: 1-2057 <MAN>
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N--EELEDDL
                                              RCVGELDEEL
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                                                                                                                                         QTSGSQHCLPKKLCLERARSPMQNVL--
                                                                                                                                                                                       KKQK----NFDKILAEEKAISEQIAQERDTAEREAREKETKVLSVSRELDEAFD-----
                                                                                                                                                                                                                                                                                     KELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELE
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                                                                                             KIEDLENKRKTLQNELDDLANTQGTADKNVHELEKAKRALESQLAELKAQ
                                            382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKGTLEAENADLATELRSVNSSRQENDRRRKQAESQIAELQVKLAE 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 190; DB 2; Length 2057; Pred. No. 0.037;
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1995
                                                                                                                                         -KKVHKVSKP----ESQLS-LGGQ
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilia

te genome sequence of the A69250; MUID:98049343

hyperthermophilic,

P.; Kaine, B.P.; sulfate-reducing

arch

chromosome segregation protein (smc1) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun

05-Dec-1997 #text_change 02-Jun-2000

C; Accession:

E69444

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RESULT 10
SQ4090
SQ4090
myosin heavy chain 3, skeletal muscle, embryonic - human
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S04090; S06146; S05442; S12466; S09333; A35082
R;Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Rubinstein, N.A.; Kelly, Nucleic Acids Res. 17, 3591-3592, 1989
A;Ritle: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.
A;Reference number: S04090; MUID:89263803
                                                                                                            FEBS Lett. 256, 21-28, 1989
A;Title: Human embryonic myosin heavy chain A;Reference number: S06146; MUID:90033298
A;Accession: S06146
A;Accession: S06146
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A;Status: preliminary; nucleic acid sequence n
A;Molecule type: DNA
A;Residues: 1-1156 <KLE>
A;Cross-references: GB:AE000995; GB:AE000782;
C;Superfamily: chromosome segregation protein
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A; Residues: 1-1940 <ELL>
A; Cross references: EMBL: X13988; NID: g34843;
R; Eller, M.; Stedman, H.H.; Sylvester, J.E.;
R; Eller, M.; Stedman, H.H.; Sylvester, J.E.;
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A;Cross-references: EMBL:X13100; NID:g31143; R;Karsch-Mizrachi, I; Travis, M.; Blau, H.; Nucleic Acids Res. 17, 6167-6179, 1989 A;Tille: Expression and DNA sequence analysis A;Reference number: S05442; MUID:89366648
                                                                                     A; Molecule type: mRNA
A; Residues: 774-1662/QT/,1665-1940 <EL2>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMNPRLHQPPFGDEIDLNTTFDVNTPPTQ----TSGSQHCLPKKLCLERARSPMQNVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- VPKIVEELDKIKEEHQRNREILISIEKKIESLEFKREQLESSMQEKQVYLDEIKDRI
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78; Conservative
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 sequence analysis of MUID:89366648
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Pred. No. 0.029;
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                                                                                                                                                                 cDNA. Interspecies
                                                                                                                                                                                                  PIDN:CAA32167.1; PID:g34844 Fertels, S.H.; Wu, Q.L.; Ra
                                                                        PIDN:CAA31492.1;
                                                       Leinwand,
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SMC1
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                    embryonic
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                                                                      PID: g31144
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A; Residues: 856-1390,
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Best Local S
Matches 77
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4
 QKQPNRTTAESRSSTDVVRI 416
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A; Residues: 856-1390, 'KK', 1393-1940 <KAR>
A; Cross-references: EMBL:X15696; NID:936504; PIDN:CAA33731.1; PID:91335313
R; Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylv, J. Biol. Chem. 265, 3568-3576, 1990
A; Title: The human embryonic myosin heavy chain. Complete primary structure A; Reference number: A35082; MUID:90154023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;549-586/Region: actin binding *status predicted F;656-678/Region: actin binding *status predicted F;840-1940/Domain: coiled coil *status predicted F;840-1280/Region: $2
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C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; ATP; coiled coil; hydrolase; methyla F;89-767/Domain: myosin motor domain homology <MMOT>
F;179-186/Region: nucleotide-binding motif A (P-loop)
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A;Accession: S09333
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A; Residues: 856-1330 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>
A; Cross-references: EMBL:X51593; NID:g29463; PIDN:CAA35942.1; PID:g294
A; Experimental source: Cross & Condde H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1281-1940/Region: light meromyosin
F;130/Modified site: N6,N6,N6-trimethyllysine (:F;185/Binding site: ATP (Lys) #status predicted
F;696,706/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 856-901,'X',903-971,'X',973-1041,'X',1043-1111,'X',1113-1181,'X',1183-125
1,'X',1673-1741,'X',1743-1811,'X',1813-1881,'X',1883-1940 <BOW>
A;Cross-references: EMBL:X51593
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                                                                                                                                                                                                                                                                               ELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKTIINKLFFDLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLE 112
ADIQLALEEAEAALEHEEAKILRIQLELTQVKSEIDRKIAEKDEEIEQLKRNYQRTV---
                                                                                                                                                                                                                                                                                                                                                                  QRTEELEEAQ----EKLAQRLQDSEEQVEAVNAKCASLEKTKQRLQGEVEDLMVDVERAN 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EENKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAH-----RLKCKMKTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNEEIQRSLSELTTQKSRLQTEAGELSRQLEEKESIVSQLSRSKQAFTQQTEELKRQLE
                                                                                                                                                                             PASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK
                                                                                                                                                                                                                                         SLAAALDKKQRNFDKVLAEWKTKCEESQAELEASLKESRSLSTELFKLKNAYEEALDQLE
                                                                                                                                                                                                                                                                                                                                                                                                                    EQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK-----
                                                        ---KLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLG
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Pred. No. 0.052;
3; Mismatches 177;
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                                                                                                                    -LEKSRKQIELEK
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                                                                                                                                                                                                                                                                                                     279
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   1595
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                                                                                                                    1538
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myosin heavy chain, skeletal muscle, embryonic - rat N; Contains: myosin ATPase (EC 3.6.1.32) C; Species: Rattus norvegicus (Norway rat) C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001 C; Accession: A24922; A22538; B24263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-1039 <STE>
A;Cross-references: EMBL:X59552; NID:g62995; PIDN:CAA42130.1; PID:g62996
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; nucleotide binding; P-loop
C;Keywords: ATP; nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
518199
myosin heavy chain - chicken (fragment)
c;Species: Gallus gallus (chicken)
c;Species: Callus gallus (chicken)
c;Accession: S18199
R;Stewart, A.F.R.; Camoretti-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, J. Mol. Evol. 33, 357-366, 1991
A; Molecule type: DNA
A; Residues: 1-1940 <STR>
A; Cross-references: GB:X
                                                                     A;Reference number: A24922; MUID:87060988 A;Accession: A24922
                                                                                                                   A; Title: Complete nucleotide and
                                                                                                                                        R;Strehler, E.E.; Strehler-Page, M.A.; Perriard, J. Mol. Biol. 190, 291-317, 1986
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A;Accession: S18199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INKLFFDLAQEEENVL - - DAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNA 116
                                                                                                                                                                                                                                                                                                                                                                                               IDSLQSTLDSEARSRNEAIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K----QRGFDKIINDWKQKYEESQAELEASQKEARSLSTELFKLKNAYEETLDHLETLKR 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDLVSSRSKLKTLN---TELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEDAKKKLLARLQEAEEA I EAANAKCSSLEKAKHRLQNEQEDMMIDLEKANSAAASLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSE--VEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLK-----EARKATGELADRLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | | | | : : | : ETMQSALDAEVRSRNEAIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEAEGALEHEESKTLRFQLELSQLKADFERKLAEKDEEMQNI - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%;
1 Similarity 20.2%;
77; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TAESRSSTDVVRI 416
  GB:X04267;
GB:X05004; NID:g56658; PIDN:CAA27817.1;
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                                                                                                                   encoded amino
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                                                                                                                   acid
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                                                                                                                                                           J.C.;
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                                                                                                                                                           M.; Nadal-Ginard,
                                                                                                                   mammalian
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PID:g1619328
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                                                                                                                myosin
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A;Introns: 68/3; 116/3; 169/1
A;Note: the list of intron positions may be incomplete
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylat
F;89-767/Domain: myosin motor domain homology cMMOT>
F;179-186/Region: actin binding #status predicted
F;656-678/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L00370; GB:M10135; NID:9205580; PIDN:AAAA1655.1; R;Periasamy, M.; Wydro, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal J. Biol. Chem. 260, 15856-15862, 1985. A;Title: Characterization of cDNA and genomic sequences corresponding to A;Reference number: A24263; MUID:86059474
A;Accession: B24263
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A;Title: Intron positions are conserved in the 5' A;Reference number: A22538; MUID:85080119
A;Accession: A22538
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F;130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status
F;185/Binding site: ATP (Lys) #status predicted
F;696,706/Active site: Cys #status predicted
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A; Residues: 1-168 <ST2>
B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone pMHC-72 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:K03468; NID:g205573; PIDN:AAA41652.1;
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A; Residues: 1358-1490,'G'
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Best Local
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                                                                                                1540 DIQMALEEAEAALEHEEAKILRIQLELTQVKSEIDRKIAEKDEEIEQLKRNYQRTV---E 1596
                                                                                                                                                                                                                                                 281
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                                                                                                                                                                                                                                  ASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EENKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAI 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERNATVESLQNALNKAEMLCSTLKKOMKFLEQRODETKOAREEAHRLKCKMKTMEQIELL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKNEETQRSLSELTTQKSRLQTEAGELSRQLEEKESIVSQLSRSKQAFTQQIEELKRQLE 1321
TMQGALDAEVRSRNEAIRL 1615
                                              KQPNRTTAESRSSTDVVRI 416
                                                                                                                                               --KLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQ
                                                                                                                                                                                                VKRENKNLEQEIADLTEQIAENGKSIHE----
                                                                                                                                                                                                                                                                                                LAAALDKKQRNFDKVLAEWKTKCEESQAELEAALKESRSLSTELFKLKNAYEEALDQLET
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19.5%;
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Pred. No. 0.059;
4; Mismatches 1
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myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum) N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Dictyostelium discoideum

RESULT A26655

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myosin heavy chain, striated adductor muscle N; Contains: myosin ATPase (EC 3.6.1.32) C:Species: Aequipecten irradians C:Date: 31-Dec-1993 #sequence_revision 31-Dec C:Accession: A40997; S13557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: The rod domain is highly periodic, containing a patter of c;Superfamily: myosin heavy chain; myosin motor domain homology c;Superfamily: myosin binding; ATP: coiled coil; hydrolase; nucleot F:1-818/Domain: globular head <HED>
F:89-747/Domain: myosin motor domain homology <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)
F:819-2116/Domain: alpha-helical rod <ROD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 2035-2116 <DEL>
R; Wagle, G.; Noegel, A.; Scheel, J.; Geris
FEBS Lett. 227, 71-75, 1988
A; Title: Phosphorylation of threonine res:
A; Reference number: S00250; MUID:88112226
A; A; Accession: S00250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change C:Accession: A26655; A24728; S00250 R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986 A;Title: Conserved protein domains in a myosin heavy chain gene A;Reference number: A26655; MUID:87092266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-2116 <WAR>
A; Cross-references: GB:M14628; GB:M11938; NID:g167834; PI
A; Cross-references: GB:M14628; GB:M11938; NID:g167834; PI
R; DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A; Reference number: A24728; MUID:86016788
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A40997
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A; Residues: 1734-1893 <WAG>
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A; Title: Complete pa
A; Reference number:
                                        R;Nyitray, L.; Goodwin, E.B.; Szent-Gyoergyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
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                  primary structure of a scallop striated muscle
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A; Molecule type: mRNA
A; Residues: 1-1938 <NYI>
A; Residues: 1-1938 <NYI>
A; Cross-references: GB:X55714; NID:g5611; PIDN:CAA39247.1;
A; Cross-references: GB:X55714; NID:g5611; PIDN:CAA39247.1;
C; Superfamily: myosin heavy chain; myosin motor domain homotor domain hydrolase; mus
C; Keywords: actin binding; ATP; coiled coil; hydrolase; mus
C; Keywords: actin binding; ATP; coiled coil; hydrolase; mus
F; 86-763/Domain: myosin motor domain homology CMMOT>
F; 86-763/Domain: myosin motor domain homology CMMOT>
F; 176-183/Region: nucleotide-binding motif A (P-loop)
A;Cross-references: GB:D10280; GB:D90237; NID:g217729; C;Superfamily: myosin heavy chain; myosin motor domain C;Keywords: ATP; smooth muscle
                                                                                                                                                            C;Accession: A38650
R;Kuro-o, M.; Nagai, R.; Nakahara,
J. Biol. Chem. 266, 3768-3773, 1991
A;Title: cDNA cloning of a myosin h
A;Reference number: A38650; MUID:91
                                                                                                                                                                                                                                                                           myosin heavy chain, embryonic smooth muscle - rabb:
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992
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                                                                                                                 A; Reference number: A. A; Accession: A38650
A; Status: preliminary
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                                                                     A; Molecule type: mRNA
A; Residues: 1-501 <KUR>
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23.0%;
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MUID:91139672
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Pred. No. 0.079;
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                                                                                                                                                                                                                                                                                20-Jun-2000
                                                                                                                                                                                       smooth muscle
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                                                PID:g217730
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A; Gene:
C; Superf
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B70356
chromosome assembly protein homolog - Aquifex aeolicus
c; Species: Aquifex aeolicus
c; Species: Aquifex aeolicus
c; Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
c; Accession: B70356
R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grah
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A; Residues: 1-1156 <AQF>
A; Cross-references: GB:AE000699; NID:g2983238;
A; Experimental source: strain VF5
                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666
A;Accession: B70356
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily:
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Best Local
                    286
                                                                                                                                                                                                                                                                         207
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                                                                                                                                                                                                                                                                                                      66 LAQEEENV----LDAEFLKNELDSVKAQLSQKDREKRDSQAIID----TLRDTLEERNATVE 119
                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NARQQLERQNKDLKAKLQELEGAVKSKFKATISALEAKIGQLEEQL
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                                                    EREKLRELEEEEERLKITFDEVKKLEEEKEKLTEKLNSLNKEKQEL--EIQRANLKNKIE
                                                                                       SRSKLKTLNTELDQAKL---ELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATN---
                                                                                                                             LINNLLSDKENLEREVGTLQLELEK - - -
                                                                                                                                                            LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVS
                                                                                                                                                                                                  ENEKELNERERLLKEVNEKIMPFKEKVGKFTAEIENAERSIKEKERELKESENRVKNLEE
                                                                                                                                                                                                                                   SLQNALNKAEMLCSTLKKQM------KFLEQRQDETKQAREEAHRLKCKMKTMEQIEL
                                                                                                                                                                                                                                                                       LKEEKEKLEKFKELQRIKRETEA-KILLKEKEKLLKERERILNELSSLRESLEDITFQIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARMRQLEEELEEEQSNMELLNDRFRK------TTLQVDTLNAELAAERSAAQKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKKLKSLEAEILQLQEELASSERARRHAEQERDEL---ADEIANSASGKSALLDEKRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNKQLRADMEDLMSSKDDVGKNVHELEKSKRALEQQVEEMRTQLEELEDELQATEDAKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                  segregation
                                                                                                                                                                                                                                                                                                                                              92;
- HMNPRLHQPPFGDEIDL-NTTFDVNTPPTQTSGSQH
                                                                                                                                                                                                                                                                                                                                            Score 181; DB 2;
Pred. No. 0.055;
02; Mismatches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182.5; DE Pred. No. 0.018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                             · LKEEYKSLKEV -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAC06839.1;
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A;Cross references: GB:M93676; NID:g212448; PIDN:AAA48985.1; PID:g212449
A;Note: sequence extracted from NCBI backbone (NCBIN:112864)
C;Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyla C;Keywords: myosin heavy chain-B, neuronal #status predicted <MYN's;1-2007/product: myosin heavy chain-B, nonmuscle #status predicted <
F;18-802/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide binding motif A (P-log)
F;178-185/Region: alternatively collected (P-log)
F;178-185/Region: alternatively col
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Accession: B43402; A43402
R;Takahashi, M.; Kawamoto, S.; Adelstein, R.S.
J. Biol. Chem. 267, 17864-17871, 1992
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F;1316-2007/Region: light meromyosin
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F;184/Binding site: ATP (Lys) #status predicted
F;732,742/Active site: Cys #status predicted
F;1954/Binding site: phosphate (Thr) (covalent) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;559-593/Region: actin binding #status predicted F;632-652/Region: alternatively spliced segment 2 #status F;692-714/Region: actin binding #status predicted
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A; Residues: 1-211; 222-631; 653-2007 <TA2>
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A; Residues: 1-2007 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession:
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                                                                  KDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNE
                                                                                                                                                                                                                                                                                      TEDAKLRLEVNMQAMKAQFERDLQARDEQNEEKKRMLVKQVRELEAELEDERKQRALAVA 1648
                                                                                                                                                                                                                                                                                                                                                      AEMICSTLKKQMKFLEQRQDETKQAREEAHRLKCKM--KTMEQIELLLQSQRSE-----
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-SEKKLKGLEAETLQLQEEFAASERARRHAEQERDEL---ADETANSASGKSALLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 181;
Pred. No. 0
                                                                                                                                                                                      -SAVEQLAVYCVSLKKEYENLKEARKATGELADRLK
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119

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A:Introns: 46/1; 192/1; 292/1; 468/2; 1921/3
C:Superfamily: myosin heavy chain; myosin motor domain }
C:Keywords: actin binding; ATP; coiled coil; hydrolase;
F:89-802/Domain: myosin motor domain homology <mMOT>
F:202-209/Region: nucleotide-binding motif A (P-loop)
F:690-712/Region: actin binding #status predicted
F:793-807/Region: actin binding #status predicted
F:875-1992/Domain: coiled coil #status predicted
F:875-1189/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myosin heavy chain A [similarity] - Caenorhabditis elegans N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans C;Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_C;Accession: T23622; S02771
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                                                                  В
                                                                                               Qy
                                                                                                                                                                                                                          F;1190-1992/Région: light meromyosin
F;153/Modified site: N6,N6,N6 trimethyllysine
F;268/Binding site: ATP (Lys) #status predicte
F;730,740/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-116,140-1992 <DIB>
A; Cross-references: EMBL: X08067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. 2015, 603-613, 1989
A:Title: Sequence analysis of the complete Caene A;Reference number: S02771; MUID:89178677
A;Accession: S02771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-1992 <WIL>
A; Cross-references: EMBL: Z78199; PIDN: CAB01576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T23622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, August
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status:
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Matches
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                                                                                                                                                        Local
ESKLSDITGQLEDMQERNEDLARQKKKTDQELSDTKKHVQDLELSLRKAEQEKQSRDHNI
                                                                                                     LQCLIQWFETAPSRTCPQCRIQVGKKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQL
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                                                                                                                                                      Similarity
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                                -DREKRDSQATIDT------LRDTLEE---RNATV 118
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us predicted
                                                                                                                                     Score 180; DB Pred. No. 0.12
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KLEEIEAAKKALQLKVQELTDTN----EGLFAKIASQEKVRFKLMQDLDDAQSD 1467
                                                                                                                                                                                                                                                                                                                                                                                                           VSRLVFESPAPVEMMNPRLHQPPFGDEIDLNT-----TFDVNTPPTQTSGSQH--- 335
                                                                                                           RQALAATAKNLEHENTILRE----HLDEEAESKADLTRQISKLNAEIQQWKARFDSEGLN 1417
                                                                                                                                                                                                                                   LQDFAALKNRLNNENSDLNRSLEEMDNQLNSLHRLKSTLQSQL----DETRRNYDEESRE 1361
                                                                                                                                                                                                                                                                                                                                                    LQKLKAKSEAEKSKLQRDLEESQHATDSEVRSRQDLEKALKTIEVQYSELQTKADEQSRQ 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGGATAAQLEANKKREAEIAKLRREKEEDSLNHETAISSLRKRHGDSVAEL---TEQLET 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLAENNSIIAKLQRLIKELTARNAELEEELEAERNSRQKSDRSRSEAERELEELTERLEQ 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEENIDREKRSRGDIEKAKRKVEGDLKVAQENIDEITKQKHDVETTLKRKEEDLHHTNA 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS
                                                                                                                                                                                                                                                                                          -----CLPKKL-----CLERARSPMQNVLKKVHKV-SKPESQLSLGGQRCVGELDEE--- 381
                                                                                                                                                                     ----LAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVVR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AKLEL-
                                              -GRTKFIQPR-----DTTIIRPVPVKSKAKSKQKVRIKTVSSASQPKLD 465
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A:Molecule type: mRNA A:Residues: 1-52, EAT, 56-659, TT, 661-868, TT, 870-930, CC, 932-1239, KG, A:Residues: B:M81105; NID:9188988; PIDN:AAA59888.1; PID:9553596 A:Cross-references: GB:M81105; NID:9188988; PIDN:AAA59888.1; PID:9553596 R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S. Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994 A;Cross-references: GB:M69180; NID:g189029; PIDN:AAA61765.1; R;Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A. Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990 A;Title: Human nonmuscle myosin heavy chain mRNA: generation A;Reference number: A34876; MUID:90138958 A;Accession: A34876 Circ. Res. 69, 530-539, 1731
A;Title: Human nonmuscle myosin heavy chains
A;Title: Human nonmuscle myosin heavy chains
A;Title: Human nonmuscle myosin heavy chains A;Cross-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036 R;Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Blood 78, 1826-1833, 1991 C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994
C;Accession: A61231; A34876; I52562; I61692 A;Title: Cellular myosin heavy chain in human A;Reference number: I52562; MUID:92003925 A;Accession: I52562 myosin heavy chain nonmuscle form A - human N;Alternate names: cellular myosin heavy chain; N;Contains: myosin ATPase (EC 3.6.1.32) A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 715-1961 <SAE> A; Molecule type: mRNA A; Residues: 1-715 <SIM> A; Reference number: A61231; A; Accession: A61231 R;Simons, M.; Wang, M.; McBride, O.W.; Circ. Res. 69, 530-539, 1991 translated from GB/EMBL/DDBJ Kawamoto, are leukocytes: myosin S.; Yamakawa, K.; Gdula, D.; encoded #text_change 19-Jan-2001 multiple type by two isolation 9: of PID:g189030 unconventional myosin diversity through genes located of 5' ,1242-1337 CDNA

on Adelste

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Arnaout,

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myosin heavy chain, nonmuscle, form IIB - )
N;Alternate names: myosin type 10; NMMHC-B
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-1
                                                                                                                    RESULT
A59252
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F:837-127/Domain: S2 *status predicted <DS2>
F:1278-1961/Domain: light mercomyosin *status predicted <LMM>
F:1278-1961/Domain: carboxyl-terminal <CBT>
F:125/Modified site: N6,N6.N6-trimethyllysine (Lys) *status F:180/Binding site: ATP (Lys) *status predicted F:694,704/Active site: Cys *status predicted
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C; Superfamily: myosin heavy chain; myosin motor domain l
C; Keywords: actin binding; ATP; coiled coil; hydrolase;
F; 84-764/Domain: myosin motor domain homology <MMOT>
F; 174-181/Region: nucleotide-binding motif A (P-loop)
F; 52-565/Region: actin binding #status predicted
F; 626-640/Region: actin binding #status predicted
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A;Cross-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134 C;Genetics:
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A;Cross-references: GDB:120216; OMIM:160775
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les 108; Conserv
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      #sequence_revision 19-May-2000 #text_change
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19.2%;
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A;Map position: 17p13-17p13
C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylat E;88-771/Domain: myosin motor domain homology <MMO>
E;18-185/Region: nucleotide-binding motif A (P-loop) E;178-185/Region: actin binding #status predicted E;533-647/Region: actin binding #status predicted E;633-647/Region: actin binding #status predicted E;129/Modified site: MTP (Lys) #status predicted E;184/Binding site: ATP (Lys) #status predicted E;701,711/Active site: Cys #status predicted
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Circ. Res. 69, 530-539, 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on
A;Reference number: A61231; MUID:91318803
A;Accession: B61231
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A; Cross-references: GB:M69181; NID:g641957; PIDN:AAA99177.1; PID:g641958
A; Experimental source: clone lib Lambda Zap II adult human T-cell library; cell line A; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between A; McLes 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides in mRNA encoding human brain MHC-B there is an a; Note: between nucleotides in mRNA encoding human brain MHC-B there is an a; Note: between nuc
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J. Muscle Res. Cell. Motil. 16, 379-389, 1995
A;Title: Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and A;Reference number: A59252; MUID:96025307
A;Accession: A59252
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A; Residues: 1-81 <WEI>
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A; Residues: 63-237, 'K', 239-664, 'L', 666-722
A; Cross-references: GB: M69181; NID: g641957
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A; Residues: 1-1976 <SIM>
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Best Local Similarity
Matches 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                       --SEKKLKSLEAEILQLQEELASSERARRHAEQERDEL---ADEITNSASGKSALLDEKR 1732
SDNARQQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQL
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                                                                                   ----KLCLERARSPMQNVLKKVHKVSKPESQLSLGG-QRCVGELDEEL
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21.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 179.5; D
Pred. No. 0.12;
'7; Mismatches
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RESULT

21

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A; Molecule type: DNA
A; Residues: 1-1017 < LIQ>
A; Residues: 1-1017 < LIQ>
A; Cross-references: GB:U25725; NID:g818866; PIDN:AAA86889.1; PID:g818867
A; Note: repeat 15-160 and 200-340
A; Note: repeat 15-160 and 200-340
C; Comment: This protein contains a coiled-coil and a globular domain at the carboxy-term C; Comment: nucleoprotein; phosphoprotein
C; Keywords: nucleoprotein; phosphoprotein
F; 465/Binding site: phosphate (Thr) (covalent) (by camp-dependent kinase) #statu
F; 465/Binding site: phosphate (Ser) (covalent) (by cAmp-dependent kinase) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-cycle-dependent 350K nuclear protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C;Accession: PC4035
R;Li, Q; Ke, Y; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.
Blochem. Biophys. Res. Commun. 212, 220-228, 1995
A;Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain A; Reference number: PC4035; MUID:95336446
                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text.
C;Accession: S21801; PN0013; S18134
R;Sun, W; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a neuronal myosin A;Reference number: S21801; MUID:92235856
                                                                                                                                                                                                                                                                                                                       myosin heavy chain, neuronal [similarity]
N;Alternate names: myosin II
N;Contains: myosin ATPase (EC 3.6.1.32)
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                                             A;Cross-references: EMBL:X62659 R;Sun, W.; Chantler, P.D.
                                                                                             A; Residues: 1-1999 <SUN>
                                                                                                                A; Molecule type:
                                                                                                                                          A; Accession: S21801
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Biophys. Res. Commun. 175, 244-249, 199
A unique cellular myosin II exhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDKVENLERELQMSEENQELVILDAENSKAEVETLKTQIEEMARSLKVFELDLVTLRSEK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKQKLEKKDEEISRLKNQIQDQEQLVSKLSQVEGEHQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENLTKQIQEKQGQLSELDKLLSSFKSQLEEKEQAEIQIKEESKTAVEMLQNQLKELNEAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKEDLTNELQKEQERISELEIINSSFENILQEKEQEKVQMKEKSSTAMEMLQTQLKSSMR
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Pred. No. 0.06
9; Mismatches
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A; Molecule type: mRNA
A; Residues: 1914-1998, / I
A; Residues: 1914-1998, / I
A; Experimental source: brain
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylat
F; 844-763; Domain: myosin motor domain homology cMMOT>
F; 174-181/Region: nucleotide-binding motif A (P-loop)
F; 174-181/Region: actin binding #status predicted
F; 336-199/Domain: coiled coil #status predicted
F; 836-199/Domain: coiled coil #status predicted
F; 836-1296/Region: Scilebt moreous
transport protein USO1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein D2552; protein YDL058w C;Species: Saccharomyces cerevisiae c;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_C;Accession: S67593; A38455; S30782
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Best Local Similarity
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                                                                                                                                                                                                            AELEAMEQKAEFLRKNLQEMTERL 1507
                                                                                                                                                                                                                                                                                                                                                                                          KKKMEDSVGCLETAEEVKRKLQKDLEGLSQRHEEKVAAYDKLEKTKTRLQQELDDLLVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK-----QMKFLEQ 144
                                                                                                                                                                                                                                                                                                DHQRQSACNLEKKQKKFD-----
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                                                                                                                                                                                                                                                        ----VGELDEEL 382
                                                                                                                                                                                                                                                                                                                                           -TTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKVSKPE
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20.9%;
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Pred. No. 0.14
%1; Mismatches
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                         12-Jul-1996 #text_change
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A;Residues: 1-1790 <BLO> A;Cross-references: EMBL:274106; NID:g1431058; A;Experimental source: strain S288C

PID:e253003;

PID:g1431059;

MIPS:YDL058

R; Bloecker, H.; Brandt, P. submitted to the Protein S A; Reference number: S67587 A; Accession: S67593 A; Molecule type: DNA

otein Sequence S67587

Database,

July

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hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) c;Speciles: Schizosaccharomyces pombe
C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38077
R;Connor, R; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, April 1996
A;Reference number: Z21767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-389, 'TAF', 392-724, 'S', 726-1790 < NAK>
A; Residues: 1-389, 'TAF', 392-724, 'S', 726-1790 < NAK>
A; Cross-references: GB: X54378; NID: g4777; PIDN: CAA38253.1; PID: g4778
A; Note: the authors translated the codon ACT for residue 768 as Ile
R; Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.
submitted to the EMBL Data Library, February 1993
A; Description: An integrin analogue in Saccharomyces cerevisiae.
A; Reference number: S30782
A; Accession: S30782
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C:Keywords: coiled coil; transmembrane protein
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A;Residues: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580,
A;Cross-references: EMBL:L03188
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A;Title: A cytoskeleton-related gene, USO1, is A;Reference number: A38455; MUID:91185402
A;Accession: A38455
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                                                                                                                                                                                                                                                                                                               FPLFIRNAVLGQKQPNRTTAESRSSTDVVRIGFDGLGGRTKFIQPRDTTIIRPVPVKSK- 444
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18.1%;
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C;Date: 22-Oct-1999 #sequence_revision
C;Accession: T30171
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Best Local Similarity
Matches 105; Conserv
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Pred. No. 0.15;
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3; Mismatches
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A;Accession: T38077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DAA
A;Residues: 1-1957 <CON>
A;Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A;Experimental source: strain 972h-; cosmid c1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-2168 <BOU>
A;Residues: 1-2168 <BOU>
A;Cross-references: EMBL:U40342; NID:glll3864; PID:glll3865; PIDN:AAA83234.1
A;Experimental source: strain C57B1/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bouckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.;
J. Cell Sci. 109, 179-190, 1996
                                                                                                                                                                                                                      31 LQCLIQWFETAPSRTCPQCRIQVGKKTIINKLFFDLAQEEENVLDAEFLK-NELDSV---
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                                                    KLEELNGSQEELWQKIETIEQEKASIQTMVEKLKKQVSDLKIKNQQLDSENIELSQKNSQ 1625
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                                                                                                           ---KAQLSQK----DREKRDSQAIIDTLR---DTLEERNATVE-----SLQNAL 125
                                                                                                                                                                  RKVELLRYESEKLQEENSILRNEITTLNEEDSISNL
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STLKKOM-KFLEQRODETKOAREEAH 157
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myosin heavy chain II - Acanthamoeba castellanii
N;Contains: myosin AfPase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-.
C;Accession: A27224
R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J. Cell Biol. 105, 913-925, 1987
A;Title: Complete nucleotide sequence and deduced polypeptide sequence A;Reference number: A27224; MUID:87308395
A;Accession: A27224
A;Molecule type: DNA
A;Cross*references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID
A;Cross*references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID
                                                                                                                                                                                                                                                                                                                 F;182-189/Region: nucleotide-binding motif Å (P-loop)
F;544-576/Region: actin binding #status predicted
F;640-682/Region: actin binding #status predicted
F;648-1227/Domain: coiled coil #status predicted <COI>
F;1228-1247/Domain: hinge <HIN>
F;1228-1247/Domain: coiled coil #status predicted <COI>
F;1248-1482/Domain: coiled coil #status predicted <CO2>
F;1483-1599/Domain: carboxyl-terminal <CBT>
F;1483-1599/Domain: carboxyl-terminal <CBT>
F;188/Binding site: NG.NG.NG-trimethyllysine (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 69/3; 119/3; 181/2
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated
F;92-775/Domain: myosin motor domain homology <MMOT>
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Best Local S
Matches 81
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                                     182
 989
                                                                                                 QNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEVE 181
                                                                                                                                                     LAEE-----DADKLEKDLAALKLKILDLEGEKAD
                                                                                                                                                                                       LAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNA----TVESL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNRTTAESRSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TEQEKLTLKRECEQSQKEQSPTS-----RKVGQMGSLERGLETIHLENEGLKKKQMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLERARSPMONVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQK--O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLVFESPAPVEMMNPRLHQPPFGDEIDLNTT-----FDVNTPPT--QTSGSQHCLPKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETESDLQVTRQEKEAVKQEVMSLHRQLQNAIDKDWVSETAP-HLSGLRGQQRRLSWDKLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKLQTHVMEQENLLLKDELERLKQLHRCPDLSDLQQKMSSVLSYNEKLLKEKEVLSEEL
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 DKYEDEAAAHD---
                                                                       EEELQEETSASNDILEQKRKLEAEKGELKASLEEEER----NRKALQEAKTKVESERNELQ
                               EMIRDMGVGQSAVEQLAVYCVSLKKEYENL~KEARKATGELAD--RLKKDLVSSRSKLKT
                                                                                                                                                                                                                           Similarity 24.1
81; Conservative
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                                                                                                                                                                                                                                               7.48;
SLKKKEEDLSRELRETKDALADAENISETL---RSKLKN 1035
                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                         Score 176.5;
Pred. No. 0.13
53; Mismatches
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                           paramyosin - nematode (Onchocerca volvulus) (fragments) C;Species: Onchocerca volvulus C;Species: Onchocerca volvulus C;Date: 14-May-1993 #sequence_revision 14-May-1993 #tex:C;Accession: B44972 R;Limberger, R.J.; McReynolds, L.A. Mol. Biochem. Parasitol. 38, Z71-280, 1990 A;Title: Filarial paramyosin: cDNA sequences from Dirof. A;Reference number: A44972; MUID:90220759 A;Accession: B44972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CES
A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1
A;Description: The sequence of C. elegans
A;Reference number: 218487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1827 <FUL>
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A;Molecule
                 A;Status:
                                                                                                                                                                                                         B44972
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Best Local
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ns: 76/2; 131/3;
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                 preliminary
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25.38;
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                                                                                                                                                   14-May-1993 #text_change
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hypothetical protein F35D11.11 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text C:Accession: T16270 R:Fulton, B.
                                                                                                                                                                                                                                                                            QVGKKT----IINKLFFDLAQEEENVLD------AEFLKNELDSVKAQLSQKDREKRD
                                                                                                                                                                                                                                                      QVNERTRQISEANEKYDDAARKNDALLEDVATWQEKYEQLKMELEEMNRRGQEKEREEAD
                                                                                                                      AREEAHRLKCKMKTMEQIEL-LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN 210
                                                                                                                                                                    LRALLDDLRGNFDKLTNELKQKGVTVDSLNEEI-----SSLKEQLNKSEKERKEELLR
                                                                                                                                                                                                            SQAIIDTLR-----DTLEERNATVESLQNALNKAEMLCSTLKKQM-KFLEQRQDETKQ
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                                                                                 MEELEQKNEAEMKEEYEVKLQLAEKDRQGVENFGKEC---EARMNELTKIHEMLMEEHDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            159/3; 185/3; 221/3; 253/3;
-RKELEKLNEQNDGDRAEWSNERNRLESSKNEAVTELQE
                                                                                                                                                                                                                                                                                                                                                           Score 176.5; D
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 1995
legans cosmid
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Dirofilaria

immitis and

Onchocerca

02-Jul-1998

GB:M29736; GB:M29737; GB:M29738; GB:M29739; motor domain homology

G

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R; Burton, J.
R; Burton, J.
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 29
T22976
hypothetical protein F59A2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22976; T23157
R;Lightning, J.
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                                                                                                              A; Map position:
A; Introns: 13/2;
                                                                                                                                             A; Gene: CESP:F59A2.6
                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                         A; Cross-references: EMBL: Z66514;
                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T23157
                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1133 <WIL>
A; Cross-references: EMBL
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A; Accession: T22976
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A; Cross-references: GB:M29734; GB:M29735;
C; Superfamily: myosin heavy chain; myosin
                                                                                                                                                                                                           A;Residues: 1-1133 <WI2>
                                                                                                                                                                                                                        A; Molecule type: DNA
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                                               Query Match
Best Local
                                Matches
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QEEENVLDAE--FLKNELDSVKAQLSQKDREKRDS-QAIIDTLRDTLEE-----
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                                                Similarity
                                                                                                                43/3;
                                  Conservative
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                                                                                                                                                                            clone
                                                                                                              107/3;
                                               7.38;
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                                  108;
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                           Score 175.5; I
Pred. No. 0.1;
08; Mismatches
                                                                                                                                                                                         PIDN:CAA91344.1; GSPDB:GN00021;
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Pred.
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                                                                                                           710/3;
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A:Gene: unc-15
A:Introns: 29/3; 55/3; 74/3; 103/3; 140/3; 159/2; 232/3; 267/3; 578/2;
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: acetylated amino end; coiled coil; phosphoprotein
E:2/Modified site: acetylated amino end (Ser) (in mature form) #status
E:6,8,14,16/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                               A; Molecule type: protein
A; Residues: 2-41;143-167;195-216;299-318;787-802;807-836
A; Note: the amino end of the mature protein is blocked
A; Note: the composition of a 32P-labeled peptide contain:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paramyosin - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 04-Dec-1992 #sequence_revision C;Accession: S04027; S05282; S04470
                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: S05282
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A; Residues: 1-866 < KAG>
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A;Accession: S04027
                                                                                                                                                                                                                                                         A; Title: Phosphorylation of A; Reference number: S04470;
                                                                                                                                                                                                                                                                                                  R; Schriefer, L.A.; Waterston, J. Mol. Biol. 207, 451-454, 19
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 'MERLESLEPLELMERMELQELLIVSLESK', 13-
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Query Match Best Local Similarity

7.3%;

Score 175; Pred. No. 0

DB 2;

Length 866

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R;Gardner, A.
submitted to the EMBL Data Library,
* Peference number: Z19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
719296
rypothetical protein F07A5.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc
C;Accession: T19296; T20541
                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z79694; PIDN:CAB01965.1; G
A;Experimental source: clone C15A11
R;Wilkinson, J.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19288
A;Accession: T20541
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                        A; Map position: 1
A; Introns: 39/3; 58/3; 87/3; 124/3; 143/2;
C; Superfamily: myosin heavy chain; myosin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z19103
A;Accession: T19296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-872 <WIL>
                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-872 <WI2>
A;Cross-references: EMBL:272506; PIDN:CAA96622.1; GSPDB:GN00019;
A;Experimental source: clone F07A5
                                                                                                                                                                                                                     A; Gene: CESP: F07A5.7
                                                                         Matches
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                                                                                          Local
                                   KLFFDLAQEEENVLDAEFLKNELDSVKAQLS-----QKDREKRDS-----
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KLHDELHEAKEALADANRKLHELDLENARLAGEIRELQTALKEADAQRRDAENRAQRALA 490
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                                                                                        Similarity
                                                                         Conservative
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                                                                                      7.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAB01965.1; GSPDB:GN00019; CESP:F07A5
                                                                                      Score 175; DB 2
Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             September
                                                                       Mismatches
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                                                                                                                                                              motor domain ho
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                                                                                                       Length 872;
                                                                     Indels
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                                                                                                                                                                               605/3;
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome segregation protein (smc1) PAB2109 - Pyrococcus abyssi (strain Orsay)
C; Species: Pyrococcus abyssi
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
B75150
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C;Superfamily: chromosome segregation protein
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A;Accession: B75150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
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A; Residues: 1-1177 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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Best Local S
Matches 88
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                                                                                                                                                                                                                                LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREE----AHRLKCKMKTMEQIELLLQSQ
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                                                  IARWGKRKEALLNKIKELEEERNKLVVKLGEIDRT---FAVAREEFDNVVKELENARKSL
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                                                                                                                        SSEEALKITREIGEVNSKINLAKRNIEVAKKELDEAQIRLIKAKDELKKVLSEIEKSKGA
                                                                                                                                                              RS-----
                                                                                                                                                                                                                                                                                                                                             88; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
                                                                                    ---KDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKS
                                                                                                                                                          -EVEEMI----RDMGVGQSAVEQLAVYCVSLKKEYEN-LKEARKATGE
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                                                                                                                                                                                                                                                                                                                                                          Score 175; DB 2; Length 1177; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                             Mismatches
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.A.; Luros, J.S.; Maitl, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21018719

A;Accession: F96673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1313 <STO>
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                                      --LDEEL--AGAFPLFIRNAVLGQKQP-NRTTAESRS
                                                                                 --KELHLMGCVKKSEEENSSSQEEVSRLVNLLKESEEDACARKEEEASLKNNLKVAEGEV 565
                                                                                                                              LPKKL----CLERAR---
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al Similarity 21.9%;
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                                                                                                                                                                         ----TNEKYEKMLEDA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 175; DB 2; L; Pred. No. 0.13; 81; Mismatches 126;
                                                                                                                            ---SPMQNVLKKVHK--VSKPESQLSLGGQRCVGE---
                                                                                                                                                                    ------RNEIDSLKSTVDSIQNEFENSKAGWEQ-
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Marziali,
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giantin - human

N;Alternate names: gcp372
C;Species: Homo sapiens (man)
C;Date: 01.Nov-1996 #sequence_revision 01.Nov-1996 #text_change 20-Aug-1999
C;Accession: 152300
R;Sohda, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ikehara, Y.
Biochem. Biophys. Res. Commun. 205, 1399-1408, 1994
A;Title: Molecular cloning and sequence analysis of a human 372-kDA protein : A;Reference number: 152300; MUID:95100974
A;Accession: 152300
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3225 eRES>
A;Cross-references: GB:D25542; NID:g662389; PIDN:BAA05025.1; PID:g808869
C;Superfamily: giantin
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26-Jan-1996

#text_change

10-Dec-1999

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RESULT 36
S00084
S00084
myosin heavy chain, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S00084; S14807
R;Maeda, K.; Sczakiel, G.; Wittinghofer, A.
Eur. J. Biochem. 167, 97-102, 1987
A;Title: Characterization of cDNA coding for the complete light meromyosin A;Reference number: S00084; MUID:87304245
A;Accession: S00084
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A;Title: Molecular genetic analyses of a 376-kilodalton Golgi comple A;Reference number: A56539; MUID:94187728
A;Accession: A56539
A;Molecule type: mRNA
A;Residues: 1-3259 <SEE-
A;Cross-references: EMBL:X75304; NID:g405714; PIDN:CAA53052.1; PID:g
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C;Superfamily: 91antin
C;Keywords: coiled coil; Golgi apparatus;
F;3238-3254/Domain: transmembrane #status
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A;Cross-references: GDB:454958
A;Map position: 3q13.31-3q13.31
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115; Conser
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Pred. No. 0.39;
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                    Conservative
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A; Molecule type: mRNA
A; Rosidues: 1-676 <mARE>
A; Cross-references: EMBL:X05958; NID:g1622; PIDN:CAA29391.1; PID:g1364242
A; Note: the sequence from Fig. 5 is inconsistent with that from Fig. 3 in R; Maeda, K.; Roesch, A.; Maeda, Y.; Kalbitzer, H.R.; Wittinghofer, A. FEBS Lett. 281, 23-26, 1991
A; Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its A; Reference number: S14807; MUID:91200294
A; Accession: S14807
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
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                                                                                                                                                                                                                                                 Cell 79, 449-458, 1994
A;Title: A heterodimeric coiled-coil protein required A;Reference number: A55094; MUID:95042742
A;Accession: B55094
                                                                                                                                                                                                                                                                                                                                                  chromosomal protein XCAP-E - African clawed frog C;Species: Xenopus Laevis (African clawed frog) C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 C;Accession: B55094 R;Hirano, T.; Mitchison, T.J.
                                                                                              A;Cross-references: GB:Ul3674; NID:g563813; PIDN:AAA64680.1; PID:g563814 C;Superfamily: chromosome segregation protein SMC1 C;Keywords: chromosomal protein; DNA condensation; heterodimer
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                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1203 <HIR>
                                                                                                                                                                                                                            A; Status: preliminary
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Best Local Similarity
Matches 80; Conserv
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21.9%;
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Score 173.5; D
Pred. No. 0.14;
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Pred. No. 0.069;
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                          DB 2;
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69;

Mismatches

135;

Indels

57;

Gaps

11;

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A;Status: preliminary
A;Nolecule type: nucleic acid
A;Nolecule type: nucleic acid
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:122784, NCBIP:122786)
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP
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A48467
A48467
Ryosin heavy chain - nematode (Brugia malayi) (fragment)
C:Species: Brugia malayi
C:Species: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
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A;Title: Myosin heavy chain is a dominant parasite antigen recognized by antibodies in
A;Reference number: A48467; MUID:93133225
A;Accession: A48467
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                                                                                                                                                                                                                                                                                                                                                                      LLEERNNVF -
ELAKLRRDLEEANMNHENQLAAIRKNNDAVAELGDQIEQAQKAKRKIEKDKIQAQRDAED
                                        HCLPKKLCLERARSPMQNVL----
                                                                                                                                               K--IGGELKVAQENMEEIERQRHEIESNLKKKESEAQAITTRLEEEQDLVGKLK--KQVN
                                                                                                                                                                                                                     KEKKHQEEINRKLMEDLQVEEDKGNYSNKLKGKLEQSLDDLEDNLEREKRGRNEIEKQKR
                                                                                                                                                                                                                                                                                              SDLSRSKKKIENDVENLKKAIADLEIRLQKTDADKQSREQQIRTLQDEMQQQDENIAKLN
                                                                                                                                                                                                                                                                                                                              ESLQNALNKAEMLCSTLKKQMKFLE---QRQDETKQAREEAHR-LKCKMKTMEQIELLLQ
                                                                        ETQNRITELEEELENERQSRSKADRAKSDLQREPEELGDRLDEQGGATAAQVEVNKKREA
                                                                                                                                                                                 KDLVSSRSKLKTLN-TELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATN
                                                                                                                                                                                                                                                           SQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE------NLKEARKATGELADRLK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERYNDLMKRKRIVENDKSKI----LTTIEELDQK 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPMONVLKKVHKVSKPESQLSLGGQRCVGELDEE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWIASEKHLFG----QANTAYDFKTNNPKEAGQRLHKLQEKKEKLGRNVNMRAMNMLTQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KETIMGHDKEIKTKSSEAGKLRENNNDLQLKIKELEHNISKHKKDSADAAAKVAKMLNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPV-EMMNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKMKNAEAERERELKEAQQKLDTAKKKADASNKKMKEKQQEVDALVL-----ELEELKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---RLHQPPFGDEIDLNTTFDVNTPPTQTSGSQ-HCLPKKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOMKFLE-QRQDETKQARE-----EAHRLKCKMKTMEQIELLLQSQRSEVEEMIRD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMKSEEAELLQTKLQQSSYHKQQEE---LDSLKQTIEESEETLKNTKEVQKKAEEKFKVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Xu, M.; Piessens, W.F
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TTYKQQIETVDEAMKAYQEQADSMASEVSKNKEAVKKAQDELAKQ
                                                                                                                                                                                                                                                                                                                                                                    -NELEAAKAQLSDVDDRLNRLSTLKTDVEKQIHELEERLGDQEDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%;
                                                                                                        -FESPAPVEMMNPRLHQPP---FGDEIDLNTTFDVNTPPTQTSGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 172.5; D
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                             184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                    -KKVHKVSKPESQLSLGGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                174
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                                                                                                            334
                                                                                                                                                 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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Eur. J. Biochem. 189, 55-65, 1990
A;Title: Identification of three developmentally controlled isoforms of A;Reference number: S09331; MUID:90235862
A;Accession: S09332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R;Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schlaffino, S.; St
Bur J. Biochem. 230, 1001-1006, 1995
A;Title: Characterization of a human perinatal myosin heavy-chain transcript.
A;Reference number: I38055; MUID:95324556
A;Accession: I38055
                                                                                                                                                    F;658-680/Region: actin binding *status predicted F;842-1282/Region: S2 *status predicted F;698,708/Active site: Cys *status predicted
                                                                                                                                                                                                                                                                                                                                  A; Map position: 17pter-17p12
C; Superfamily: myosin heavy chain; myosin motor domain l
C; Keywords: actin binding; ATP; coiled coil; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 860-969,'Q',971-1246,'H',1248-1260,'G',1262-1296,'Q',1298-1503,'AH',1506-
A;Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Feghali, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A;Title: Molecular genetic characterization
A;Reference number: A30220, MUID:89234168
A;Accession: A30220
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 502-547,'X',549-617,'X',619-687,'X',689-757,'X',759-827,'X',829-897,'X',8
-1376,'NT',1379-1386,'X',1388-1456,'X',1458-1526,'X',1528-1596,'X',1598-1666,'X',1668
A;Cross-references: EMBL:X51592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937
A; Cross-references: EMBL:x51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A; Experimental source: clone gtMHC-F
R; Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H. Eur., J. Biochem. 189, 55-65, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-14, 'A', 16-859 <KAR>
A; Cross-references: GB: Y00821
A; Experimental source: skeletal muscle
R; Bober, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z38133; NID:q558668; PIDN:CAA86293.1; PID:q558669 R;Karsch-Mizrachi, I.; Feghali, R.; Shows, T.B.; Leinwand, L.A. Gene 89, 289-294, 1990 A;Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA A;Reference number: JH0154; MUID:90323631 A;Accession: JH0154
                                                                                                                                                                                                                                                                            F;91-769/Domain: myosin motor domain homology F;181-188/Region: nucleotide-binding motif A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: S12459
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                                                                                                                                                                                                                                            F;551-588/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:125267; OMIM:160741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: MYH8
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C;Date: 17-May-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1937 < RES>
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                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVAQIDGETAAR - - - - MNNEKL - SKQYEMQIAELQTKCD
                            7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library, January
Score 172.5; DI
Pred. No. 0.27;
79; Mismatches 1
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S09332; A30220; S49478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB/EMBL/DDBJ
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                                                               1937;
                                                                                                                                                                                                                                                                                                                                        contraction; nucleotid
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Matches

Similarity 77; Conserv

Conservative

79;

167;

Gaps

9;

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hypothetical protein F5E19_70 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C:Accession: T51505 R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, submitted to the Protein Sequence Database, August 2000 A;Reference number: 25394 A;Accession: T51505 A;Status: preliminary
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A; Introns: 6/2; 79/3
A; Note: F5E19_70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-853 <SAT>
A; Cross-references: EMBL: AL391147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1386 TE--ELEEAKKKLAQRLQEAEEHVEAVNAKCASLEKTKQRLQNEVEDLMLDVERSNAACA 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1326 TKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAIQR 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
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                      246
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                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                 382 VAKQKE---DLEVSEQRLGSVEEEVSKNEKEVEKLKSELETVK---EEKNRALKKEQDAT 435
                                                                                                                                                                                                                                                                                                                              66 LAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
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  AKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPR 305
                                                         YVKKMEEDVASMGKEMNRLDNLLKRTEEEADAAWKKEAQTKDSLKEVEEEIVYLQETLGE
                                                                                                                                                                                                                                                          NKAEMLCSTLKKQMKFLE---QRQDETKQARE-----EAHRLKCKMKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDKKQRNFDKVLSEWKQK-----YEETQAELEASQKESRSLSTELFKVKNVYEESLDQL 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LADRLKK--DLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQRLINDL---TAQRARLQTEAGEYSRQLDEKDALVSQLSRSKQASTQQIEELKHQLEEE
                                                                                                                                                                       ---MEQIELLLQSQRSEVEEMI----RDMGVGQSAVEQLAVYCVSLKKEYENLKEAR---
                                                                                                                                                                                                                     SRVQRLSEEKSKLLSDLESSKEEEEKSKKAMESLASALHEVSSEGRELKEKLLSQGDHEY 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQK 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETLRRENKNLQQEISDLTEQIAEGGKQIHE------LEKIKKQVEQEKCE 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEER 114
                                                                                                                                        ETQIDDLKLVIKATNEKYENMLDEARHEIDVLVSAVEQTKKHFESSKKDWE-MKEANLVN
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 7.2%; Score 171.5; D
19.7%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                 -KATGELADRLKKDLVSSRSKLKTLNTE-----LDQ
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                                                                                                                                                                                                                                                                                                                                                                                148;
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